Available online at www.sciencedirect.com
ScienceDirect
Journal of Experimental Animal Science 43 (2007) 319–327
Journal of Experimental Animal Science
www.elsevier.de/jeas

Recessive yellow in the Mongolian gerbil (*Meriones unguiculatus*)

F. Petrij*, M. Mettler, V. Brückmann, K. van Veen

Department of Clinical Genetics, Erasmus Medical Center, Rotterdam, Westzeedijk 112, 3016 AH Rotterdam, The Netherlands

Accepted 24 September 2006

Abstract

A new autosomal recessive coat color mutant in the Mongolian gerbil (*Meriones unguiculatus*) is described: recessive yellow. On the dorsal side the mutant has a rich yellow to ginger color. Ventrally it shows the typical creamy white belly of a wild-type Mongolian gerbil. The dorsal yellow hairs have short black tips, and a light olive green base. A clear demarcation line between dorsal and ventral color is present. Crosses between recessive yellow animals and multiple homozygous recessive tester animals (*a*/*a*; c^{chm}/c^{chm}; *g*/*g*; *p*/*p*) resulted only in animals of an agouti (wild-type) phenotype, showing that the new allele is not allelic with any of the known coat color mutations in the Mongolian gerbil. Molecular studies showed that the new mutant is caused by a missence mutation at the extension (*E*) locus. On a non-agouti background (*a*/*a*; *e*/*e*) mutant animals look like a dark wild-type agouti. In contrast to wild-type agouti it shows yellow pigmentation and dark ticking at the ventral side, resulting in the absence of a demarcation line. Since black pigment is present in both the agouti and non-agouti variant (*A*/*A*; *e*/*e* and *a*/*a*; *e*/*e*), we conclude that recessive yellow in the Mongolian gerbil is non-epistatic to agouti. Additionally we describe a second mutation at the same locus leading to a similar phenotype, however without black pigment and diminishing yellow pigment during life. Fertility and viability of both new mutants are within normal range. The extension (*E*) gene is known to encode the melanocortin 1 receptor

*Corresponding author. Tel.: +31 10 463 6915; fax: +31 10 436 7133.
E-mail address: f.petrij@erasmusmc.nl (F. Petrij).

doi:10.1016/j.jeas.2006.09.006

(MC1R). Interestingly, this is the only gene that is known to account for substantial variation in skin and hair color in humans. Many different mutations are known of which some are associated with higher skin cancer incidence.

Keywords: Mongolian gerbil; Meriones; Coat color; Extension locus; Melanocortin 1 Receptor (MC1R); Recessive yellow; Fading recessive yellow

Introduction

In March 1993 we received several gerbils from the Zoological gardens of Poznan (Poland), where they were kept as an unknown gerbil species. No further information about the origin of the animals was available. Karyotyping at the University of Lübeck (Germany), taxonomic investigations at the Museum Alexander Koenig, Bonn (Germany), and breeding experiments showed the animals to be conspecific with *Meriones unguiculatus* (type specimens are stored at the Museum Alexander Koenig in Bonn). We concluded that these animals represent a new coat color mutation of the Mongolian gerbil.

This mutation showed to be not allelic with other known coat color mutations and is caused by a missense mutation at the extension locus. The extension gene is known to encode the melanocyte-stimulating hormone receptor (MC1R) (Robbins et al., 1993) in which a loss-of-function causes exclusive production of red/yellow pheomelanin, and a constitutively activating mutation causes exclusive production of black/brown eumelanin, reviewed in Jackson (1993) and Barsh (1996). Mutations at the extension locus are known in many different mammals such as rabbits, Syrian hamsters, Guinea pigs (Robinson, 1978), mice (Silvers, 1979), horses (Marklund et al., 1996), cattle (Klungland et al., 1995; Joerg et al., 1996), dogs (Newton et al., 2000), foxes (Vage et al., 1997), pigs (Kijas et al., 1998) as well as in humans (Valverde et al., 1995).

Despite a large number of murine (and to a lesser extent gerbil) coat-color mutations, the only gene in humans that is known to account for substantial variation in skin and hair color is the melanocortin 1 receptor gene (*MC1R*). Most persons with red hair are homozygous for alleles of the *MC1R* gene that show varying degrees of diminished function. More than 65 human *MC1R* alleles with nonsynonymous changes have been identified. Some of these alleles are associated with higher skin cancer incidence (Rees, 2004).

Known gerbil coat colors

The typical agouti (wild-type) phenotype of the Mongolian gerbil is characterized by dorsal hairs with a gray base, a yellow center band and black tips (see Fig. 1A). The belly and paws are creamy white. A demarcation line between dorsal and ventral side is present. The eyes, claws, and the tip of the tail are black.